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RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,405

TIME: 14:44:34

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Output Set: N:\CRF3\02152002\J056405.raw

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3 <110> APPLICANT: ZWIEBEL, LAURENCE J.  
 5 <120> TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF  
 6 USE THEREOF  
 8 <130> FILE REFERENCE: N7841  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/056,405  
 C--> 11 <141> CURRENT FILING DATE: 2002-01-24  
 13 <150> PRIOR APPLICATION NUMBER: 60/264,649  
 14 <151> PRIOR FILING DATE: 2001-01-26  
 16 <160> NUMBER OF SEQ ID NOS: 23  
 -18 <170> SOFTWARE: PatentIn Ver. 2.1  
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 21 <211> LENGTH: 1964  
 22 <212> TYPE: DNA  
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 28 aaatcaaccg agctaacaaa caacatccctg tgcaaaatct agcagtgaag gtgtgatatc 180  
 29 gtatacctgt acctgtaaac cgttgtgctg gtgtgtgctt ttgtgtatca attttgtgga 240  
 30 aaacagaaaa tacatcaaaa tgggtttaca tttcaaagtc ttcaagaagt gcgcccctaa 300  
 31 tggaaagggtt acgctgtaca tgggcaagcg tgactttgta gaccacgttt ccggcggttg 360  
 32 accgatcgat ggtatcgctg tcctcgatga tgagtacatt cgtgacaacc gtaagggtatt 420  
 33 cggtcagatt gtctgcagtt tccgctacgg ccgcgaagag gacgaggtga tgggactaaa 480  
 34 cttccagaag gagttatgcc tcgcttccga acagatctac ccgcgtccgg aaaagtcgga 540  
 35 caaggagcag accaagctcc aggagcgact gctgaagaag ctgggttcga acgccatccc 600  
 36 gtacacgttc aacatctcgc cgaatgctcc gtcttcggtc acgctgcagc agggcggaag 660  
 37 tgataatgga gaccgtgctg gtgtgtcgta ctacgtgaag atctttgccg gtgagtcgga 720  
 38 aaccgatcgt acgcaccgtc gcagcaccgt tacgctcggc atacgaaga tccagttcgc 780  
 39 accgaccaag cagggccagc agccgtgcac gctggtgctg aaggacttta tgctaagccc 840  
 40 gggagagctg agctcgagg tcacactaga caagcagctg tacctgcagc gggagcgaat 900  
 41 aggcgtcaac atctgcaccc gcaacaactc gaacaaaatg gtcaagaaga ttaaggccat 960  
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54 cacatgttcc ccagcgagcg gtaactgttc tgttctgaca ccttcgctc gacaatgtac 1740
55 cttttaaaaa catacaaatt agaagtcgtc ttactacct tcaaccaatc cagccacttt 1800
56 ggtatatact tttcatagaa tccttctgag cgcaaggacc ctattgaaat tcagtgttat 1860
57 tttgtaactg cgaccaaatt cctagctgaa tgttgttgaa cgagttatgt acatcaaaag 1920
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70 Val Thr Leu Tyr Met Gly Lys Arg Asp Phe Val Asp His Val Ser Gly
71 20 25 30
73 Val Glu Pro Ile Asp Gly Ile Val Val Leu Asp Asp Glu Tyr Ile Arg
74 35 40 45
76 Asp Asn Arg Lys Val Phe Gly Gln Ile Val Cys Ser Phe Arg Tyr Gly
77 50 55 60
79 Arg Glu Glu Asp Glu Val Met Gly Leu Asn Phe Gln Lys Glu Leu Cys
80 65 70 75 80
82 Leu Ala Ser Glu Gln Ile Tyr Pro Arg Pro Glu Lys Ser Asp Lys Glu
83 85 90 95
85 Gln Thr Lys Leu Gln Glu Arg Leu Leu Lys Lys Leu Gly Ser Asn Ala
86 100 105 110
88 Ile Pro Phe Thr Phe Asn Ile Ser Pro Asn Ala Pro Ser Ser Val Thr
89 115 120 125
91 Leu Gln Gln Gly Glu Asp Asp Asn Gly Asp Pro Cys Gly Val Ser Tyr
92 130 135 140
94 Tyr Val Lys Ile Phe Ala Gly Glu Ser Glu Thr Asp Arg Thr His Arg
95 145 150 155 160
97 Arg Ser Thr Val Thr Leu Gly Ile Arg Lys Ile Gln Phe Ala Pro Thr
98 165 170 175
100 Lys Gln Gly Gln Gln Pro Cys Thr Leu Val Arg Lys Asp Phe Met Leu
101 180 185 190
103 Ser Pro Gly Glu Leu Glu Leu Glu Val Thr Leu Asp Lys Gln Leu Tyr
104 195 200 205
106 Leu His Gly Glu Arg Ile Gly Val Asn Ile Cys Ile Arg Asn Asn Ser
107 210 215 220
109 Asn Lys Met Val Lys Lys Ile Lys Ala Met Val Gln Gln Gly Val Asp
110 225 230 235 240
112 Val Val Leu Phe Gln Asn Gly Ser Tyr Arg Asn Thr Val Ala Ser Leu
113 245 250 255
115 Glu Thr Ser Glu Gly Cys Pro Ile Gln Pro Gly Ser Ser Leu Gln Lys
116 260 265 270
118 Val Met Tyr Leu Thr Pro Leu Leu Ser Ser Asn Lys Gln Arg Arg Gly
119 275 280 285
121 Ile Ala Leu Asp Gly Gln Ile Lys Arg Gln Asp Gln Cys Leu Ala Ser
122 290 295 300
124 Thr Thr Leu Leu Ala Gln Pro Asp Gln Arg Asp Ala Phe Gly Val Ile

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125 305          310          315          320
127 Ile Ser Tyr Ala Val Lys Val Lys Leu Phe Leu Gly Ala Leu Gly Gly
128          325          330          335
130 Glu Leu Ser Ala Glu Leu Pro Phe Val Leu Met His Pro Lys Pro Gly
131          340          345          350
133 Thr Lys Ala Lys Val Ile His Ala Asp Ser Gln Ala Asp Val Glu Thr
134          355          360          365
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137          370          375          380
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141 <211> LENGTH: 1239
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147 ttgcagttgc tttgtttgaa atatttaggc ctatggccac cggaagatac ggatcaggca 120
148 acgcggaacc ggtacatcgc gtacggttgg gctttgcgga tcatgtttct acatctgtac 180
149 gctctaacgc aagccctata cttcaaggat gtgaaggata ttaatgacat cgcaaatgca 240
150 ttgttcgtgc ttatgactca agtgacgttg atctacaagc tggaaaagt ttaactacaac 300
151 atcgcacgga ttcagggttg tctgcgcaag ctttaactgca cactgtatca cccgaaacag 360
152 cgcaagaat tcagcccgtg tttacaatcg atgagtggag tgttttggct gatgatcttt 420
153 ctcatgtttg tggctatctt caccatcatc atgtggggtta tgtcgccagc cttcgacaat 480
154 gaacgtcgtc tgcccgtgcc ggccgtggtc ccggtggact atcaccattc ggacatagtg 540
155 tacggtgtac tgttcctgta tcaaaccatt ggaatcgtca tgagcgcaac gtacaacttc 600
156 tcgaccgata ccatgttttc cggcttgatg ctacacataa atggacaaat tgtgcggctt 660
157 ggtagtatgg ttaaaaagct tggacatgac gtccctcccg aacgccaatt ggtcgcaacg 720
158 gatgcggaat ggaagagat gcgaaagcgc atcgaccatc actccaaagt gtacggtacg 780
159 atgtacgcta aagtaacgga gtgtgtgctg ttccacaagg acatcttaag gatctatctt 840
160 cgcgcaagta tgcgcgtctg taattatcat ttgtatgaca ctgctgcaac taccgggggc 900
161 gatgttacga tggccgatct gctgggctgt ggggtctatt tgctagtaaa gacatcgcaa 960
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163 tttgttgggt tttccaacta cttcaagttc gataagcgta ccagccaagc aatgatattt 1080
164 tttctgcaaa tgactcttaa agatgttcac atcaagggtg gaagtgtctt gaaggttacg 1140
165 ctaaatcttc acacattttt gcagattatg aagctatcgt actcctatct ggccgtactt 1200
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179 20 25 30
181 Tyr Ile Ala Tyr Gly Trp Ala Leu Arg Ile Met Phe Leu His Leu Tyr
182 35 40 45
184 Ala Leu Thr Gln Ala Leu Tyr Phe Lys Asp Val Lys Asp Ile Asn Asp
185 50 55 60
187 Ile Ala Asn Ala Leu Phe Val Leu Met Thr Gln Val Thr Leu Ile Tyr

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190 Lys Leu Glu Lys Phe Asn Tyr Asn Ile Ala Arg Ile Gln Ala Cys Leu
191          85          90          95
193 Arg Lys Leu Asn Cys Thr Leu Tyr His Pro Lys Gln Arg Glu Glu Phe
194          100         105         110
196 Ser Pro Val Leu Gln Ser Met Ser Gly Val Phe Trp Leu Met Ile Phe
197          115         120         125
199 Leu Met Phe Val Ala Ile Phe Thr Ile Ile Met Trp Val Met Ser Pro
200          130         135         140
202 Ala Phe Asp Asn Glu Arg Arg Leu Pro Val Pro Ala Trp Phe Pro Val
203 145          150         155         160
205 Asp Tyr His His Ser Asp Ile Val Tyr Gly Val Leu Phe Leu Tyr Gln
206          165         170         175
208 Thr Ile Gly Ile Val Met Ser Ala Thr Tyr Asn Phe Ser Thr Asp Thr
209          180         185         190
211 Met Phe Ser Gly Leu Met Leu His Ile Asn Gly Gln Ile Val Arg Leu
212          195         200         205
214 Gly Ser Met Val Lys Lys Leu Gly His Asp Val Pro Pro Glu Arg Gln
215          210         215         220
217 Leu Val Ala Thr Asp Ala Glu Trp Lys Glu Met Arg Lys Arg Ile Asp
218 225          230         235         240
220 His His Ser Lys Val Tyr Gly Thr Met Tyr Ala Lys Val Thr Glu Cys
221          245         250         255
223 Val Leu Phe His Lys Asp Ile Leu Arg Ile Tyr Leu Arg Ala Ser Met
224          260         265         270
226 Arg Val Cys Asn Tyr His Leu Tyr Asp Thr Ala Ala Thr Thr Gly Gly
227          275         280         285
229 Asp Val Thr Met Ala Asp Leu Leu Gly Cys Gly Val Tyr Leu Leu Val
230          290         295         300
232 Lys Thr Ser Gln Val Phe Ile Phe Cys Tyr Val Gly Asn Glu Ile Ser
233 305          310         315         320
235 Tyr Thr Asp Lys Phe Thr Glu Phe Val Gly Phe Ser Asn Tyr Phe Lys
236          325         330         335
238 Phe Asp Lys Arg Thr Ser Gln Ala Met Ile Phe Phe Leu Gln Met Thr
239          340         345         350
241 Leu Lys Asp Val His Ile Lys Val Gly Ser Val Leu Lys Val Thr Leu
242          355         360         365
244 Asn Leu His Thr Phe Leu Gln Ile Met Lys Leu Ser Tyr Ser Tyr Leu
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247 Ala Val Leu Gln Ser Met Glu Ser Glu Glx
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252 <211> LENGTH: 1142
253 <212> TYPE: DNA
254 <213> ORGANISM: Anopheles gambiae
256 <400> SEQUENCE: 5
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259 aacgttttcc agttcctgaa gctgtactcg tcctggggcg acatgagcga gctcatcatc 180

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260 aacggataact ttaccgtgct gtactttaac ctcgtcctcc gaacctcctt tctcgtgac 240
261 aatcgacgga aatttgagac attttttgaa ggcgttgccg ccgagtacgc tctcctogag 300
262 aaaaatgacg acatccgacc cgtgctggag cggtagacac ggcggggacg catgctatcg 360
263 atatcgaatc tgtggtctgg cgccttcatt agtgectgct ttgtgacctt tctctgttt 420
264 gtgcccgggc gcgccctacc gtacggcgctc acgataccgg gcgtggacgt gctggccacc 480
265 ccgacctacc aggtcgtgtt tgtgctgcag gtttacctta ccttccccgc ctgctgcatg 540
266 tacatcccgt tcaccagctt ctacgcgacc tgcacgctgt ttgcgctcgt ccagatagcg 600
267 gccctaaagc aacggctcgg acgcttgggg cgccacagcg gcacgatggc ttcgaccgga 660
268 cacagcgccg gcacactggt cgccgagctg aaggagtgtc taaagtatca caaacaatc 720
269 atccaatatg ttcagtatct caactcactc gtcacccatc tgtgtctgct ggagttcctg 780
270 tcgttcggga tgatgctgtg cgcactgctg tttctgctaa gcattagcaa tcagctggca 840
271 cagatgataa tgattggatc gtacatcttc atgatactct cgcagatgtt tgcttctat 900
272 tggcatgcga acgaggtact ggagcagagc ctaggcattg gcgatgccat ttacaatgga 960
273 gcgtggccgg actttgagga accgataagg aaacggttga ttctaattat tgcacgtgct 1020
274 cagcgaccga tggtggtgta attaaagtcg gcaacgtgta cccgatgacg ttggaaatgt 1080
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289 20 25 30
291 Gly Cys Ile Pro Val Ala Val Leu Asn Val Phe Gln Phe Leu Lys Leu
292 35 40 45
294 Tyr Ser Ser Trp Gly Asp Met Ser Glu Leu Ile Ile Asn Gly Tyr Phe
295 50 55 60
297 Thr Val Leu Tyr Phe Asn Leu Val Leu Arg Thr Ser Phe Leu Val Ile
298 65 70 75 80
300 Asn Arg Arg Lys Phe Glu Thr Phe Phe Glu Gly Val Ala Ala Glu Tyr
301 85 90 95
303 Ala Leu Leu Glu Lys Asn Asp Asp Ile Arg Pro Val Leu Glu Arg Tyr
304 100 105 110
306 Thr Arg Arg Gly Arg Met Leu Ser Ile Ser Asn Leu Trp Leu Gly Ala
307 115 120 125
309 Phe Ile Ser Ala Cys Phe Val Thr Tyr Pro Leu Phe Val Pro Gly Arg
310 130 135 140
312 Gly Leu Pro Tyr Gly Val Thr Ile Pro Gly Val Asp Val Leu Ala Thr
313 145 150 155 160
315 Pro Thr Tyr Gln Val Val Phe Val Leu Gln Val Tyr Leu Thr Phe Pro
316 165 170 175
318 Ala Cys Cys Met Tyr Ile Pro Phe Thr Ser Phe Tyr Ala Thr Cys Thr
319 180 185 190
321 Leu Phe Ala Leu Val Gln Ile Ala Ala Leu Lys Gln Arg Leu Gly Arg
322 195 200 205
324 Leu Gly Arg His Ser Gly Thr Met Ala Ser Thr Gly His Ser Ala Gly

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date